IFWO

RAW SEQUENCE LISTING DATE: 07/26/2004
PATENT APPLICATION: **US/10/810,262** TIME: 14:42:58

Input Set : **A:\67452029.app**
Output Set: **N:\CRF4\07262004\J810262.raw**

<110> APPLICANT: NAYLOR, STUART
KINGSMAN, SUSAN MARY
BINLEY, KATIE
<120> TITLE OF INVENTION: POLYNUCLEOTIDE CONSTRUCTS AND USES THEREOF
<130> FILE REFERENCE: 674523-2029.1
<140> CURRENT APPLICATION NUMBER: 10/810,262
<141> CURRENT FILING DATE: 2004-03-26
<150> PRIOR APPLICATION NUMBER: 09/787,562
<151> PRIOR FILING DATE: 2001-07-06
<150> PRIOR APPLICATION NUMBER: PCT/GB99/03181
<151> PRIOR FILING DATE: 1999-09-22
<150> PRIOR APPLICATION NUMBER: PCT/GB98/02885
<151> PRIOR FILING DATE: 1998-09-23
<150> PRIOR APPLICATION NUMBER: GB 9901906.9
<151> PRIOR FILING DATE: 1999-01-28
<150> PRIOR APPLICATION NUMBER: GB 9903538.8
<151> PRIOR FILING DATE: 1999-02-16
<160> NUMBER OF SEQ ID NOS: 34
<170> SOFTWARE: PatentIn Ver. 3.2
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<213> ORGANISM: Artificial Sequence
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ccatagtccc gcccctaact ccgcccatcc cgcccctaac tccgcccagt tccgcccatt 180
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73 <220> FEATURE:
74 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
75 oligonucleotide construct
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79 gtcgtgcagg acgtgacatc tagagaacca tcagatgttt ccagggtgcc ccaaggacct 120
80 gaaatgaccc tgtgccttat ttgaactaac caatcagttc gcttctcgct tctgttcgcg 180
81 cgcttctgct ccccgagctc aataaaagag cccacaaccc ctcactcgg 229
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85 <211> LENGTH: 225
86 <212> TYPE: DNA
87 <213> ORGANISM: Artificial Sequence
89 <220> FEATURE:
90 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
91 oligonucleotide construct
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95 acgtcctgca cgactctaga gaaccatcag atgtttccag ggtgccccaa ggacctgaaa 120
96 tgaccctgtg ccttatttga actaaccaat cagttcgctt ctcgcttctg ttcgcgcgct 180
97 tctgctcccc gagctcaata aaagagccca caacccctca ctcgg 225
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101 <211> LENGTH: 633
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103 <213> ORGANISM: Homo sapiens
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107 agcccaagcg ggaccggctc ccacagccac cgcgacttcc agcccgtgct gcacctggtg 120
108 gccctgaaca gccccctgag cggcggcatg cgcggcatca ggggcgctga cttccagtgc 180
109 ttccagcagg ccagggccgt gggcctggcc ggcaccttcc gcgccttcct gagcagccgc 240
110 ctgcaggacc tgtacagcat cgtgcgcagg gccgaccgcg ctgccgtgcc catcgtgaac 300
111 ctgaaggacg agctgctgtt ccccagctgg gaggccctgt tcagcggcag cgagggcccc 360
112 ctgaagccag gcgccaggat cttcagcttc gacggcaagg acgtgctgcg ccaccccacc 420
113 tggccccaga agagcgtgtg gcacggctcc gaccccaacg gccgcaggct gaccgagagc 480
114 tactgcgaga cctggcgcac cgaggccccc agcgccaccg ggcaggccag ctccctgctg 540
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122 <213> ORGANISM: Homo sapiens
124 <220> FEATURE:
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126 <222> LOCATION: (1)..(633)
128 <400> SEQUENCE: 7

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133 gca gtc ttc gtt tcg ccc agc ggt acc gga tcc cac agc cac cgc gac   96
134 Ala Val Phe Val Ser Pro Ser Gly Thr Gly Ser His Ser His Arg Asp
135              20                  25                  30
137 ttc cag ccg gtg ctc cac ctg gtt gcg ctc aac agc ccc ctg tca ggc   144
138 Phe Gln Pro Val Leu His Leu Val Ala Leu Asn Ser Pro Leu Ser Gly
139          35                  40                  45
141 ggc atg cgg ggc atc cgc ggg gcc gac ttc cag tgc ttc cag cag gcg   192
142 Gly Met Arg Gly Ile Arg Gly Ala Asp Phe Gln Cys Phe Gln Gln Ala
143      50                  55                  60
145 cgg gcc gtg ggg ctg gcg ggc acc ttc cgc gcc ttc ctg tcc tcg cgc   240
146 Arg Ala Val Gly Leu Ala Gly Thr Phe Arg Ala Phe Leu Ser Ser Arg
147  65                  70                  75                  80
149 ctg cag gac ctg tac agc atc gtg cgc cgt gcc gac cgc gca gcc gtg   288
150 Leu Gln Asp Leu Tyr Ser Ile Val Arg Arg Ala Asp Arg Ala Ala Val
151                 85                  90                  95
153 ccc atc gtc aac ctc aag gac gag ctg ctg ttt ccc agc tgg gag gct   336
154 Pro Ile Val Asn Leu Lys Asp Glu Leu Leu Phe Pro Ser Trp Glu Ala
155             100                 105                 110
157 ctg ttc tca ggc tct gag ggt ccg ctg aag ccc ggg gca cgc atc ttc   384
158 Leu Phe Ser Gly Ser Glu Gly Pro Leu Lys Pro Gly Ala Arg Ile Phe
159         115                 120                 125
161 tcc ttt gac ggc aag gac gtc ctg agg cac ccc acc tgg ccc cag aag   432
162 Ser Phe Asp Gly Lys Asp Val Leu Arg His Pro Thr Trp Pro Gln Lys
163     130                 135                 140
165 agc gtg tgg cat ggc tcg gac ccc aac ggg cgc agg ctg acc gag agc   480
166 Ser Val Trp His Gly Ser Asp Pro Asn Gly Arg Arg Leu Thr Glu Ser
167 145                 150                 155                 160
169 tac tgt gag acg tgg cgg acg gag gct ccc tcg gcc acg ggc cag gcc   528
170 Tyr Cys Glu Thr Trp Arg Thr Glu Ala Pro Ser Ala Thr Gly Gln Ala
171                 165                 170                 175
173 tcc tcg ctg ctg ggg ggc agg ctc ctg ggg cag agt gcc gcg agc tgc   576
174 Ser Ser Leu Leu Gly Gly Arg Leu Leu Gly Gln Ser Ala Ala Ser Cys
175             180                 185                 190
177 cat cac gcc tac atc gtg ctc tgc att gag aac agc ttc atg act gcc   624
178 His His Ala Tyr Ile Val Leu Cys Ile Glu Asn Ser Phe Met Thr Ala
179         195                 200                 205
181 tcc aag tag                                                     633
182 Ser Lys
183     210
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187 <211> LENGTH: 210
188 <212> TYPE: PRT
189 <213> ORGANISM: Homo sapiens
191 <400> SEQUENCE: 8
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193   1               5                  10                  15
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195 Ala Val Phe Val Ser Pro Ser Gly Thr Gly Ser His Ser His Arg Asp
196              20                  25                  30
198 Phe Gln Pro Val Leu His Leu Val Ala Leu Asn Ser Pro Leu Ser Gly
199          35                  40                  45
201 Gly Met Arg Gly Ile Arg Gly Ala Asp Phe Gln Cys Phe Gln Gln Ala
202      50                  55                  60
204 Arg Ala Val Gly Leu Ala Gly Thr Phe Arg Ala Phe Leu Ser Ser Arg
205  65                  70                  75                  80
207 Leu Gln Asp Leu Tyr Ser Ile Val Arg Arg Ala Asp Arg Ala Ala Val
208                  85                  90                  95
210 Pro Ile Val Asn Leu Lys Asp Glu Leu Leu Phe Pro Ser Trp Glu Ala
211             100                 105                 110
213 Leu Phe Ser Gly Ser Glu Gly Pro Leu Lys Pro Gly Ala Arg Ile Phe
214         115                 120                 125
216 Ser Phe Asp Gly Lys Asp Val Leu Arg His Pro Thr Trp Pro Gln Lys
217     130                 135                 140
219 Ser Val Trp His Gly Ser Asp Pro Asn Gly Arg Arg Leu Thr Glu Ser
220 145                 150                 155                 160
222 Tyr Cys Glu Thr Trp Arg Thr Glu Ala Pro Ser Ala Thr Gly Gln Ala
223                 165                 170                 175
225 Ser Ser Leu Leu Gly Gly Arg Leu Leu Gly Gln Ser Ala Ala Ser Cys
226             180                 185                 190
228 His His Ala Tyr Ile Val Leu Cys Ile Glu Asn Ser Phe Met Thr Ala
229         195                 200                 205
231 Ser Lys
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237 <211> LENGTH: 912
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243 tccccctccg gcaccgggag cctgttcgag aagaaggtgt acctgagcga gtgcaagacc 120
244 ggcaacggca agaactacag gggcaccatg agcaagacca agaacggcat cacctgccag 180
245 aagtggagca gcaccagccc ccacaggcct cgcttcagcc ccgccaccca ccccagcgag 240
246 ggcctggagg agaactactg ccgcaacccc gacaacgacc cccagggccc ttggtgctac 300
247 accaccgacc ctgagaagcg ctacgactac tgcgacatcc tggagtgcga ggaagagtgt 360
248 atgcactgca gcggggagaa ctacgacggc aagatcagca agaccatgag cggcctggag 420
249 tgccaggcct gggactccca gagccccac gcccacggct acatccccag caagttcccc 480
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251 ttcaccaccg atcccaacaa gcgctgggag ctgtgcgaca tcccccgctg caccacccc 600
252 ccacccagca gcggccccac ctaccagtgc ctgaagggca ccggcgagaa ttaccgcggc 660
253 aacgtggccg tgaccgtgag cggccacacc tgccagcact ggagcgccca gacccccac 720
254 acccacaacc gcacccccga gaacttcccc tgcaagaacc tcgacgagaa ttattgccgg 780
255 aaccctgacg gcaagagggc cccctggtgc cacaccacca acagccaggt gcgctgggag 840
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261 <211> LENGTH: 912
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263 <213> ORGANISM: Homo sapiens
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272   1               5                  10                  15
274 gca gtc ttc gtt tcg ccc agc ggt acc gga tcc tta ttt gaa aag aaa   96
275 Ala Val Phe Val Ser Pro Ser Gly Thr Gly Ser Leu Phe Glu Lys Lys
276             20                  25                  30
278 gtg tat ctc tca gag tgc aag act ggg aat gga aag aac tac aga ggg   144
279 Val Tyr Leu Ser Glu Cys Lys Thr Gly Asn Gly Lys Asn Tyr Arg Gly
280         35                  40                  45
282 acg atg tcc aaa aca aaa aat ggc atc acc tgt caa aaa tgg agt tcc   192
283 Thr Met Ser Lys Thr Lys Asn Gly Ile Thr Cys Gln Lys Trp Ser Ser
284     50                  55                  60
286 act tct ccc cac aga cct aga ttc tca cct gct aca cac ccc tca gag   240
287 Thr Ser Pro His Arg Pro Arg Phe Ser Pro Ala Thr His Pro Ser Glu
288 65                  70                  75                  80
290 gga ctg gag gag aac tac tgc agg aat cca gac aac gat ccg cag ggg   288
291 Gly Leu Glu Glu Asn Tyr Cys Arg Asn Pro Asp Asn Asp Pro Gln Gly
292                 85                  90                  95
294 ccc tgg tgc tat act act gat cca gaa aag aga tat gac tac tgc gac   336
295 Pro Trp Cys Tyr Thr Thr Asp Pro Glu Lys Arg Tyr Asp Tyr Cys Asp
296             100                 105                 110
298 att ctt gag tgt gaa gag gaa tgt atg cat tgc agt gga gaa aac tat   384
299 Ile Leu Glu Cys Glu Glu Glu Cys Met His Cys Ser Gly Glu Asn Tyr
300         115                 120                 125
302 gac ggc aaa att tcc aag acc atg tct gga ctg gaa tgc cag gcc tgg   432
303 Asp Gly Lys Ile Ser Lys Thr Met Ser Gly Leu Glu Cys Gln Ala Trp
304     130                 135                 140
306 gac tct cag agc cca cac gct cat gga tac att cct tcc aaa ttt cca   480
307 Asp Ser Gln Ser Pro His Ala His Gly Tyr Ile Pro Ser Lys Phe Pro
308 145                 150                 155                 160
310 aac aag aac ctg aag aag aat tac tgt cgt aac ccc gat agg gag ctg   528
311 Asn Lys Asn Leu Lys Lys Asn Tyr Cys Arg Asn Pro Asp Arg Glu Leu
312                 165                 170                 175
314 cgg cct tgg tgt ttc acc acc gac ccc aac aag cgc tgg gaa ctt tgc   576
315 Arg Pro Trp Cys Phe Thr Thr Asp Pro Asn Lys Arg Trp Glu Leu Cys
316             180                 185                 190
318 gac atc ccc cgc tgc aca aca cct cca cca tct tct ggt ccc acc tac   624
319 Asp Ile Pro Arg Cys Thr Thr Pro Pro Pro Ser Ser Gly Pro Thr Tyr
320         195                 200                 205
322 cag tgt ctg aag gga aca ggt gaa aac tat cgc ggg aat gtg gct gtt   672
323 Gln Cys Leu Lys Gly Thr Gly Glu Asn Tyr Arg Gly Asn Val Ala Val
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VERIFICATION SUMMARY DATE: 07/26/2004
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